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## SEQUENCE LISTING

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<110> Luche, Ralf M.
      Wei, Bo
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<141> 2003-09-08
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tcccagcagc ggattcacca tctcaaaacc tgacaagaca tttcaaagaa agtattaaat
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ccaggagegt gacactggtg ategeataca teatgacegt cactgaettt ggetgggagg
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tgctgtggag gtttctgtac ctcgcttgga tgcctgtaag gatcccggga gccttgccgc
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His Ile Leu Ser Val His Asp Ser Ala Arg Pro Met Leu Glu Gly Val
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Lys Tyr Leu Cys Ile Pro Ala Ala Asp Ser Pro Ser Gln Asn Leu Thr
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Arg His Phe Lys Glu Ser Ile Lys Phe Ile His Glu Cys Arg Leu Arg
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Gly Glu Ser Cys Leu Val His Cys Leu Ala Gly Val Ser Arg Ser Val
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Thr Leu Val Ile Ala Tyr Ile Met Thr Val Thr Asp Phe Gly Trp Glu
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Asp Ala Leu His Thr Val Arg Ala Gly Arg Ser Cys Ala Asn Pro Asn
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       115
Val Gly Phe Gln Arg Gln Leu Gln Glu Phe Glu Lys His Glu Val His
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Gln Tyr Arg Gln Trp Leu Lys Glu Glu Tyr Gly Glu Ser Pro Leu Gln
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Phe Trp Ala Phe Leu Arg Arg Leu
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Asn Ile Leu Ala Tyr Leu Met
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DSP-3

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Glu Phe Gly Ile Lys Tyr Ile Leu Asn Val Thr Pro Asn Leu Pro Asn
Leu Phe Glu Asn Ala Gly Glu Phe Lys Tyr Lys Gln Ile Pro Ile Ser
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Asp His Trp Ser Gln Asn Leu Ser Gln Phe Phe Pro Glu Ala Ile Ser
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Phe Ile Asp Glu Ala Arg Gly Lys Asn Cys Gly Val Leu Val His Cys
          100
                              105
Leu Ala Gly Ile Ser Arg Ser Val Thr Val Thr Val Ala Tyr Leu Met
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Gly Ile Lys Tyr Ile Leu Asn Val Thr Pro Asn Leu Pro Asn Ala Phe
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Glu His Gly Gly Glu Phe Thr Tyr Lys Gln Ile Pro Ile Ser Asp His
                                      75
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Trp Ser Gln Asn Leu Ser Gln Phe Phe Pro Glu Ala Ile Ser Phe Ile
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Asp Glu Ala Arg Ser Lys Lys Cys Gly Val Leu Val His Cys Leu Ala
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                              105
Gly Ile Ser Arg Ser Val Thr Val Thr Val Ala Tyr Leu Met Gln Lys
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                          120
                                             125
Met Asn Leu Ser Leu Asn Asp Ala Tyr Asp Phe Val Lys Arg Lys Lys
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                          40
Thr Gln Asn Gly Ile Ser Tyr Val Leu Asn Ala Ser Asn Ser Cys Pro
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Lys Pro Asp Phe Ile Cys Glu Ser Arg Phe Met Arg Val Pro Ile Asn
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                                      75
Asp Asn Tyr Cys Glu Lys Leu Leu Pro Trp Leu Asp Lys Ser Ile Glu
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Phe Ile Asp Lys Ala Lys Leu Ser Ser Cys Gln Val Ile Val His Cys
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                              105
Leu Ala Gly Ile Ser Arg Ser Ala Thr Ile Ala Ile Ala Tyr Ile Met
                          120
                                              125
       115
Lys Thr Met Gly Met Ser Ser Asp Asp Ala Tyr Arg Phe Val Lys Asp
                       135
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                           155
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                           40
Gln Ala Cys Gly Ile Thr Ala Val Leu Asn Val Ser Ala Ser Cys Pro
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Asn His Phe Glu Gly Leu Phe His Tyr Lys Ser Ile Pro Val Glu Asp
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Asn Gln Met Val Glu Ile Ser Ala Trp Phe Gln Glu Ala Ile Ser Phe
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Ile Asp Ser Val Lys Asn Ser Gly Gly Arg Val Leu Val His Cys Gln
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Ala Gly Ile Ser Arg Ser Ala Thr Ile Cys Leu Ala Tyr Leu Ile Gln
                          120
                                             125
Ser His Arg Val Arg Leu Asp Glu Ala Phe Asp Phe Val Lys Gln Arg
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                                          140
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Asp Ala Leu Gly Ile Thr Ala Leu Ile Asn Val Ser Ala Asn Cys Pro
                                          60
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Asn His Phe Glu Gly His Tyr Gln Tyr Lys Ser Ile Pro Val Glu Asp
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                   70
Asn His Lys Ala Asp Ile Ser Ser Trp Phe Asn Glu Ala Ile Asp Phe
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Ile Asp Ser Ile Lys Asn Ala Gly Gly Arg Val Phe Val His Cys Gln
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                               105
           100
Ala Gly Ile Ser Arg Ser Ala Thr Ile Cys Leu Ala Tyr Leu Met Arg
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                                      125
        115
Thr Asn Arg Val Lys Leu Asp Glu Ala Phe Glu Phe Val Lys Gln Arg
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                        40
 Asp Ala Leu Gly Ile Thr Ala Leu Leu Asn Val Ser Ser Asp Cys Pro
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 Asn His Phe Glu Gly His Tyr Gln Tyr Lys Cys Ile Pro Val Glu Asp
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 Asn His Lys Ala Asp Ile Ser Ser Trp Phe Met Glu Ala Ile Glu Tyr
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 Ile Asp Ala Val Lys Asp Cys Arg Gly Arg Val Leu Val His Cys Gln
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        100
 Ala Gly Ile Ser Arg Ser Ala Thr Ile Cys Leu Ala Tyr Leu Met Met
                                                125
                            120
       115
 Lys Lys Arg Val Arg Leu Glu Glu Ala Phe Glu Phe Val Lys Gln Arg
   130
                        135
 Arg Ser Ile Ile Ser Pro Asn Phe Ser Phe Met Gly Gln Leu Leu Gln
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 Phe Glu Ser Gln Val Leu Ala Thr Ser
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<212> PRT

## <213> Homo sapien

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<210> 18 <211> 180 <212> PRT <213> Homo sapien

180

<400> 18

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His Ile Leu Ser Val His Asp Ser Ala Arg Pro Met Leu Glu Gly Val
                            40
Lys Tyr Leu Cys Ile Pro Ala Ala Asp Ser Pro Ser Thr Arg His Phe
                        55
Lys Glu Ser Ile Lys Phe Ile His Glu Cys Arg Leu Arg Gly Glu Ser
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                                        75
Cys Leu Val His Cys Leu Ala Gly Val Ser Arg Ser Val Thr Leu Val
                85
                                    90
Ile Ala Tyr Ile Met Thr Val Thr Asp Phe Gly Trp Glu Asp Ala Leu
                                105
                                                     110
His Thr Val Arg Ala Gly Arg Ser Cys Ala Asn Pro Asn Val Gly Phe
                                                125
                            120
Gln Arg Gln Leu Gln Glu Phe Glu Lys His Glu Val His Gln Tyr Arg
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Gln
145
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acacacattc tttctgtgca cgatactgcc aggcccatgt tggagggagt taaatacctg
tgtattccag cggcagacac accatctcaa aacctgacaa gacatttcaa agaaagcatt
                                                                        240
aaattcattc atgagtgccg actccagggt gagagctgtc ttgtacattg cctggctggg
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qtctccaqqa qtqtqacatt qqtqatcqca tacatcatga ctgtcaccga ctttggctgg
                                                                        360
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gaagatgcct tgcacactgt tcgtgcgggg aggtcctgtg ccaaccccaa cctgggcttt
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caaaqqcaqc tqcaqqaqtt tqaqaaacat qaaqtqcacc agtatcggca atggctgaga
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qaaqaqtatq qaqaqaaccc tttqcqqqat qcaqaaqaaq ccaaaaatat tctqgqtaaa
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tataaagagc aagggcgcat ggagccccgg cctagcagca ggcggtggag cagcttctca
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His Ile Leu Ser Val His Asp Thr Ala Arg Pro Met Leu Glu Gly Val
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Lys Tyr Leu Cys Ile Pro Ala Ala Asp Thr Pro Ser Gln Asn Leu Thr
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Arg His Phe Lys Glu Ser Ile Lys Phe Ile His Glu Cys Arg Leu Gln
                                        75
                    70
Gly Glu Ser Cys Leu Val His Cys Leu Ala Gly Val Ser Arg Ser Val
                                    90
Thr Leu Val Ile Ala Tyr Ile Met Thr Val Thr Asp Phe Gly Trp Glu
                                                    110
                                105
Asp Ala Leu His Thr Val Arg Ala Gly Arg Ser Cys Ala Asn Pro Asn
                                                125
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Leu Gly Phe Gln Arg Gln Leu Gln Glu Phe Glu Lys His Glu Val His
                                            140
                       135
Gln Tyr Arg Gln Trp Leu Arg Glu Glu Tyr Gly Glu Asn Pro Leu Arg
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                   150
Asp Ala Glu Glu Ala Lys Asn Ile Leu Gly Lys Tyr Lys Glu Gln Gly
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                                    170
               165
Arg Met Glu Pro Arg Pro Ser Ser Arg Arg Trp Ser Ser Phe Ser Thr
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Leu Pro Pro Leu Thr Tyr Asn Asn Tyr Thr Thr Glu Thr
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                                                                       180
gccaggccta tgttggaggg agttaaatac ctgtgcatcc cagcagcgga ttcaccatct
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caaaacctga caagacattt caaagaaagt attaaattca ttcacgagtg ccggctccgc
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ggtgagaget gccttgtaca ctgcctggcc ggggtctcca ggagcgtgac actggtgatc
gcatacatca tgaccgtcac tgactttggc tgggaggatg ccctgcacac cgtgcgtgct
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gggagatect gtgccaacce caacgtggge ttccagagac agetecagga gtttgagaag
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catgaggtcc atcagtatcg gcagtggctg aaggaagaat atggagagag ccctttgcag
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ctcagaagac tgtaa
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      receptor which is used as a substrate for
      phosphatase activity.
<221> PHOSPHORYLATION
<222> (5)...(5)
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